



IFW0

RAW SEQUENCE LISTING

DATE: 08/04/2004

PATENT APPLICATION: US/10/824,231

TIME: 08:33:32

Input Set : N:\CrF3\RULE60\10824231.raw

Output Set: N:\CRF4\08042004\J824231.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Palmer, Leslie M.

7 (ii) TITLE OF INVENTION: Novel ribG

10 (iii) NUMBER OF SEQUENCES: 7

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Dechert Price & Rhoads

14 (B) STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre

15 (C) CITY: Philadelphia

16 (D) STATE: PA

17 (E) COUNTRY: US

18 (F) ZIP: 19103

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Diskette

22 (B) COMPUTER: IBM Compatible

23 (C) OPERATING SYSTEM: DOS

24 (D) SOFTWARE: FastSEQ for Windows Version 2.0

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/10/824,231

C--> 28 (B) FILING DATE: 14-Apr-2004

W--> 34 (C) CLASSIFICATION:

36 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/09/376,633

33 (B) FILING DATE: 18-AUG-1999

37 (A) APPLICATION NUMBER: 08/978,456

38 (B) FILING DATE:

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Dickinson, Todd Q

44 (B) REGISTRATION NUMBER: 28,354

45 (C) REFERENCE/DOCKET NUMBER: P50444-9

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: 215-994-2252

49 (B) TELEFAX: 215-994-2222

50 (C) TELEX:

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 1029 base pairs

57 (B) TYPE: nucleic acid

58 (C) STRANDEDNESS: double

59 (D) TOPOLOGY: linear

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

64 ATGGATTATG CGATTCAACT TGCAAATATG GTACAAGGTC AAACAGGTGT TAATCCACCC 60

65 GTTGGCGCTG TTGTAGTTAA TGAAGGTAGG ATTGTTGGTA TTGGTGCACA CTTGAGAAAA 120

ENTERED

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66 GGTGACAAGC ATGCGGAGGT TCAAGCACTT GATATGGCAC AACAAAATGC TGAAGGTGCG 180
67 ACGATTTATA TTACGTTAGA GCCATGTAGT CATTTTGGTT CAACACCACC CTGTGTTAAC 240
68 AAAATTATTG ATTGTAAGAT AGCAAAAGTA GTATACGCAA CAAAAGACAA TTCGTTAGAC 300
69 ACACATGGTG ATGAGACGTT ACGGGCTCAC GGTATTGAGG TTGAATGCGT TGATGATGAA 360
70 CGGGCATCAC AATTATACCA AGACTTTTTT AAAGCAAAAG CAAAGCAACT GCCACAAATT 420
71 ACAGTGAAAAG TATCTGCAAG TTTAGATGGT AAACAAGCGA ATGATAATGG ACAAAGTCAA 480
72 TGGATTACTA ACAAAGAGGT TAAACAAGAT GTCTATAAGT TAAGACATCG ACACGACGCA 540
73 GTGTAACTG GAAGACGTAC AGTTGAATTA GATGATCCAC AATATACTAC ACGTATTCAA 600
74 GATGGAAAAA ACCCTATAAA AGTAATATTG TCTAAGTCTG GGAATATTCA TTTTAATCAG 660
75 CAAATTTATC AAGATGAATC AACACCAATT TGGATATATA CTGAAAATCC AAATTTAACA 720
76 AGCAATCAAA CACATATTGA AATTATTTAC TTGAAGTCTT GTGATTTAAC AACAATTCTT 780
77 CACAATTTAT ATAAAAGAGG AGTTGGAAC TTGCTAGTCG AGGCAGGTCC AACCCTACT 840
78 TCAGAATTCT CCATCTATTA TATAGATGAA TTTATTCTCT ATTATGCCCC GAAATTAATT 900
79 GGCGGATCTG GAAATTATCA ATTTTATCAA ACAAATGATG TGATTGAGAT ACCAGATGCG 960
80 AACCAATTTG AAATTGTTCA TTCCGAGTTA TTAAATCAAA ATGTTAAATT AACTTTACGA 1020
81 AAGAAGTGA 1029

```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

94 Met Asp Tyr Ala Ile Gln Leu Ala Asn Met Val Gln Gly Gln Thr Gly
95 1 5 10 15
96 Val Asn Pro Pro Val Gly Ala Val Val Val Asn Glu Gly Arg Ile Val
97 20 25 30
98 Gly Ile Gly Ala His Leu Arg Lys Gly Asp Lys His Ala Glu Val Gln
99 35 40 45
100 Ala Leu Asp Met Ala Gln Gln Asn Ala Glu Gly Ala Thr Ile Tyr Ile
101 50 55 60
102 Thr Leu Glu Pro Cys Ser His Phe Gly Ser Thr Pro Pro Cys Val Asn
103 65 70 75 80
104 Lys Ile Ile Asp Cys Lys Ile Ala Lys Val Val Tyr Ala Thr Lys Asp
105 85 90 95
106 Asn Ser Leu Asp Thr His Gly Asp Glu Thr Leu Arg Ala His Gly Ile
107 100 105 110
108 Glu Val Glu Cys Val Asp Asp Glu Arg Ala Ser Gln Leu Tyr Gln Asp
109 115 120 125
110 Phe Phe Lys Ala Lys Ala Lys Gln Leu Pro Gln Ile Thr Val Lys Val
111 130 135 140
112 Ser Ala Ser Leu Asp Gly Lys Gln Ala Asn Asp Asn Gly Gln Ser Gln
113 145 150 155 160
114 Trp Ile Thr Asn Lys Glu Val Lys Gln Asp Val Tyr Lys Leu Arg His
115 165 170 175
116 Arg His Asp Ala Val Leu Thr Gly Arg Arg Thr Val Glu Leu Asp Asp
117 180 185 190
118 Pro Gln Tyr Thr Thr Arg Ile Gln Asp Gly Lys Asn Pro Ile Lys Val
119 195 200 205

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120 Ile Leu Ser Lys Ser Gly Asn Ile His Phe Asn Gln Gln Ile Tyr Gln
121      210      215      220
122 Asp Glu Ser Thr Pro Ile Trp Ile Tyr Thr Glu Asn Pro Asn Leu Thr
123      225      230      235      240
124 Ser Asn Gln Thr His Ile Glu Ile Ile Tyr Leu Lys Ser Cys Asp Leu
125      245      250      255
126 Thr Thr Ile Leu His Asn Leu Tyr Lys Arg Gly Val Gly Thr Leu Leu
127      260      265      270
128 Val Glu Ala Gly Pro Thr Thr Thr Ser Glu Phe Ser Ile Tyr Tyr Ile
129      275      280      285
130 Asp Glu Phe Ile Leu Tyr Tyr Ala Pro Lys Leu Ile Gly Gly Ser Gly
131      290      295      300
132 Asn Tyr Gln Phe Tyr Gln Thr Asn Asp Val Ile Glu Ile Pro Asp Ala
133      305      310      315      320
134 Asn Gln Phe Glu Ile Val His Ser Glu Leu Leu Asn Gln Asn Val Lys
135      325      330      335
136 Leu Thr Leu Arg Lys Lys
137      340

```

139 (2) INFORMATION FOR SEQ ID NO: 3:

141 (i) SEQUENCE CHARACTERISTICS:

142 (A) LENGTH: 1269 base pairs

143 (B) TYPE: nucleic acid

144 (C) STRANDEDNESS: double

145 (D) TOPOLOGY: linear

148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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150 AANACCAAT CCNATTGGGA GGNAATCCAA ATCAATNCCC GGANNCCCAA TCCAAGTTAA      60
151 TTAAGTCCAA GGTTTTGGAA CATTACCAA TATGATTCCG ATGAGGTCAA ATGNCAANCG      120
152 GTGTTAATAA ACTACGAAAT GNTGTGNAAG TGATAGTAGA NCAAGTTGCG CATACAGTNT      180
153 CTCNATTATA TGATGCTTTA GAATCGAATG AGCAACAACA GCGCAGTTAC AATCAATAAT      240
154 TTGTAAGTAG AAGATAATAA AGAGAACGCT CTATAGAGAC GAATTGAAGG TTTGATTTTA      300
155 ATGTCTGTGA GTAAGAATCA TATCAATGAG ATGCCTATAG TACTCAGATT ATATTAAATT      360
156 AAAACCGTCA TTAATTGTTT TTTTAGAAAA CATATAGTAT CATTTTAAAT GTAGTTGACA      420
157 TACTACGTAC TCAAATAATC TATAACAATT TCATATATAA TTCTTTCGGG GCAGGGTGAA      480
158 ATTCCCAACC GGCAGTAAAT AAAGCCTGCG ACCTGCTAAT ATGTTTCATA TTAGTGGCTG      540
159 ATCTAGTGAG ATTCTAGAGC CGACAGTTAA AGTCTGGATG GGAGAAAGAA TGTTAATTAT      600
160 CGACAAAGAT AATGTAGCGT ATTTGTAAAA ATGTGTACAA ATAGGCTTAT TTAACGATAA      660
161 ATTTTCTCTC TTTGCATCTT AATTCATGAT GTGAGGATTT TTTGTTTATA GAGGTGATCA      720
162 TTTGAGTCAA TTTATGGATT ATGCGATTCA ACTTCCAAAT ATGGTACAAG GTCANACAGG      780
163 TGTTAATCCA CCCGTTGGCG CTGTTGTAGT TAATGAAGGT AGGATTGTTG GTATTGGTGC      840
164 ACACCTGAGA AAAGGTGACA AGCATGCGGA GGTTCAAGCA CTTGATATGG CACAACANAA      900
165 TGCTGAAGGT GCGACGATTT ATATTACGTT AGAGCCATGT AGTCATTTTG GTTCAACACC      960
166 ACCCTGTGTT AACAAAATTA TTGATTGTAA GATAGCANAA GTAGTATTAC NCAACANAAG      1020
167 ACAATTCCGT TAGACACACA TGGGTGATGA GACGTTACGG GGCTCCACGG TATTTGAGGG      1080
168 TTGAATTGCG TTGGATGATG AACGGGCATC ACAATTATAC CAAAGACTTT TTTTAAAGCA      1140
169 AAAAGCAAAG CAACTTGCCA CAAAATTACA GTGAAAGTNT CTTGAAAGTT TAGATGGGTA      1200
170 AACAAAGCGA ATTGATAATG GACAAAGTCA ATGGATTACT AACAAAGAGG TTAAACAAGA      1260
171 TGTCTATAG      1269

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173 (2) INFORMATION FOR SEQ ID NO: 4:

175 (i) SEQUENCE CHARACTERISTICS:

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176          (A) LENGTH: 99 amino acids
177          (B) TYPE: amino acid
178          (C) STRANDEDNESS: single
179          (D) TOPOLOGY: linear
182      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
W--> 184  Met Asp Tyr Ala Ile Gln Leu Pro Asn Met Val Gln Gly Xaa Thr Gly
185      1          5          10          15
186  Val Asn Pro Pro Val Gly Ala Val Val Val Asn Glu Gly Arg Ile Val
187      20          25          30
188  Gly Ile Gly Ala His Leu Arg Lys Gly Asp Lys His Ala Glu Val Gln
189      35          40          45
190  Ala Leu Asp Met Ala Gln Xaa Asn Ala Glu Gly Ala Thr Ile Tyr Ile
191      50          55          60
192  Thr Leu Glu Pro Cys Ser His Phe Gly Ser Thr Pro Pro Cys Val Asn
193      65          70          75          80
194  Lys Ile Ile Asp Cys Lys Ile Ala Xaa Val Val Leu Xaa Asn Xaa Arg
195      85          90          95
196  Gln Phe Arg
199  (2) INFORMATION FOR SEQ ID NO: 5:
201      (i) SEQUENCE CHARACTERISTICS:
202          (A) LENGTH: 21 base pairs
203          (B) TYPE: nucleic acid
204          (C) STRANDEDNESS: single
205          (D) TOPOLOGY: linear
208      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
210  ATGAAGGTAG GATTGTTGGT A                                     21
212  (2) INFORMATION FOR SEQ ID NO: 6:
214      (i) SEQUENCE CHARACTERISTICS:
215          (A) LENGTH: 22 base pairs
216          (B) TYPE: nucleic acid
217          (C) STRANDEDNESS: single
218          (D) TOPOLOGY: linear
221      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
223  AGTCTTGGTA TAATTGTGAT GC                                     22
225  (2) INFORMATION FOR SEQ ID NO: 7:
227      (i) SEQUENCE CHARACTERISTICS:
228          (A) LENGTH: 3336 base pairs
229          (B) TYPE: nucleic acid
230          (C) STRANDEDNESS: double
231          (D) TOPOLOGY: linear
234      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
236  ATGGATTATG CGATTCAACT TGCAAATATG GTACAAGGTC AAACAGGTGT TAATCCACCC      60
237  GTTGGCGCTG TTGTAGTTAA TGAAGGTAGG ATTGTTGGTA TTGGTGCACA CTTGAGAAAA      120
238  GGTGACAAGC ATGCGGAGGT TCAAGCACTT GATATGGCAC AACAAAATGC TGAAGGTGCG      180
239  ACGATTTATA TTACGTTAGA GCCATGTAGT CATTTTGGTT CAACACCACC CTGTGTTAAC      240
240  AAAATTATTG ATTGTAAGAT AGCAAAAGTA GTATACGCAA CAAAAGACAA TTCGTTAGAC      300
241  ACACATGGTG ATGAGACGTT ACGGGCTCAC GGTATTGAGG TTGAATGCGT TGATGATGAA      360
242  CGGGCATCAC AATTATACCA AGACTTTTTT AAAGCAAAAG CAAAGCAACT GCCACAAATT      420
243  ACAGTGAAAG TATCTGCAAG TTTAGATGGT AAACAAGCGA ATGATAATGG ACAAAGTCAA      480

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244	TGGATTACTA	ACAAAGAGGT	TAAACAAGAT	GTCTATAAGT	TAAGACATCG	ACACGACGCA	540
245	GTGTTAACTG	GAAGACGTAC	AGTTGAATTA	GATGATCCAC	AATATACTAC	ACGTATTCAA	600
246	GATGGAAAAA	ACCCTATAAA	AGTAATATTG	TCTAAGTCTG	GGAATATTCA	TTTTAATCAG	660
247	CAAATTTATC	AAGATGAATC	AACACCAATT	TGGATATATA	CTGAAAATCC	AAATTTAACA	720
248	AGCAATCAAA	CACATATTGA	AATTATTTAC	TTGAAGTCTT	GTGATTTAAC	AACAATTCTT	780
249	CACAATTTAT	ATAAAAAGAG	AGTTGGAAGT	TTGCTAGTCG	AGGCAGGTCC	AACCACTACT	840
250	TCAGAATTCT	CCATCTATTA	TATAGATGAA	TTTATTCTCT	ATTATGCCCC	GAAATTAATT	900
251	GGCGGATCTG	GAAATTATCA	ATTTTATCAA	ACAAATGATG	TGATTGAGAT	ACCAGATGCG	960
252	AACCAATTTG	AAATTGTTCA	TTCCGAGTTA	TTAAATCAAA	ATGTTAAATT	AACCTTACGA	1020
253	AAGAAGTGAT	GATGCATGTT	TACTGGCATC	GTTGAAGAAA	TAGGTGTCGT	TAAAAGTGTT	1080
254	CAAATTCGTC	AATCAGTCAG	GACGATTGAA	ATCGAAGCAC	ATAAGATTAC	GGCAGATATG	1140
255	CATATTGGTG	ATTCCATCAG	TGTTAATGGT	GCATGTTTAA	CAGTGATTGA	TTTTGATCAG	1200
256	ACATCTTTTA	CTGTTCAAGT	AATTTAAAGC	ACTGAAAATA	AAACCTATTT	AGCAGATGTT	1260
257	AAGCGACAAT	CAGAAGTAAA	TTTAGAGCGT	GCCATGAGTG	GTAACGGTAG	GTTTGGTGGA	1320
258	CATTTTGTCC	TCGGTCATGT	AGATGAACTA	GGAACAGTTT	CAAAAATAAA	TGAAACAGCC	1380
259	AATGCCAAAA	TTATTACGAT	TCAATGTAGC	CAACATATTA	ATAATCAGTT	AGTTAAGCAA	1440
260	GGGTCTATTA	CTGTGGATGG	TGTAAGTCTA	ACGGTATTTG	ATAAGCATGA	TAACAGTTTT	1500
261	GACATTCATC	TTATTCCAGA	AACGAGGCGT	TCAACGATTT	TATCATCCAA	AAAATTAGGA	1560
262	GATAAAGTAC	ATTTAGAAAC	AGACGTTTTG	TTTAAATATG	TTGAAAATAT	TTTAAATAAA	1620
263	GATAAAGACC	AATTATCTGT	AGATAAATTA	AGAGCATTTG	GTTTTTAGGA	GGGGTAGCAT	1680
264	GCAATTTCAT	AATATTGACA	GTGCTTTAAT	GGCTTTAAAA	AATGGAGAAA	CAATTATTGT	1740
265	AGTAGATGAT	GAGAATCGTG	AAAATGAAGG	TGATTTAGTA	GCGGTTACTG	AATGATGAA	1800
266	CGATAATACC	ATTAATTTTA	TGGCGAAAGA	AGCAAGGGGA	TTAATATGCG	CACCAGTGTC	1860
267	TAAAGATATT	GCACAACGTT	TGGATTTGGT	ACAAATGGTT	GATGATAACT	CCGACATCTT	1920
268	TGGTACGCAA	TTTACAGTGA	GTATTGATCA	TGTAGATACA	ACAACAGGAA	TTAGTGCTTA	1980
269	TGAACGTACA	TTGACTGCCA	AAAAGCTCAT	TGATCCTAGT	AGTGAAGCTA	AAGATTTTAA	2040
270	TCGTCTGGT	CATTTATTTT	CATTAGTAGC	ACAAGATAAA	GGCGTATTAG	CTAGAAATGG	2100
271	ACACACAGAA	GCGGCTGTTG	ATTTAGCTAA	ACTTACTGGT	GCCAAGCCCC	CTGGTGTCAT	2160
272	TTGTGAGATT	ATGAATGATG	ACGGCACGAT	GGCGAAAGGA	CAAGATTTAC	AAAATTTTAA	2220
273	AGAAAAACAT	CAATTAAAGA	TGATTACGAT	TGATGATTTA	ATTGAATATC	GTAAAAAATT	2280
274	AGAACCAGAA	ATTGAATTTA	AGGCAAAAGT	GAAAATGCCT	ACAGATTTTC	GAACATTTGA	2340
275	TATGTATGGT	TTTAAAGCGA	CATACACAGA	TGAAGAGATA	GTTGTACTGA	CAAAAGGTGC	2400
276	AATTCGACAA	CATGAAAATG	TACGCTTACA	TTCTGCGTGC	CTTACAGGCG	ATATTTTCCA	2460
277	TAGTCAACGT	TGTGATTGTG	GTGCTCAACT	TGAATCGTCT	ATGAAGTATA	TCAATGAACA	2520
278	TGGTGGCATG	ATTATTTATC	TACCTCAAGA	AGGTCGTGGC	ATAGGATTGT	TAAACAAATT	2580
279	ACGCGCATAT	GAATTAATTG	AGCAAGGATA	TGATACAGTA	ACTGCAAATT	TAGCATTAGG	2640
280	TTTTGATGAA	GATTTACGAG	ATTATCATAT	TGCTGCACAG	ATTTTAAAAAT	ATTTTAACAT	2700
281	CGAACATATC	AATTTATTAA	GTAATAATCC	AAGTAAATTT	GAGGGATTAA	AACAATATGG	2760
282	CATTGATATT	GCAGAAAGAA	TTGAAGTTAT	CGTACCAGAA	ACGGTACATA	ATCATGATTA	2820
283	TATGGTAACG	AAAAAAATAA	AAATGGGTCA	TTTAATATAG	GAGGACTTTA	ACATGAATTT	2880
284	TGAAGGTAAG	TTAATTGGAA	AAGATTTGAA	AGTTGCAATC	GTAGTTAGTC	GATTTAATGA	2940
285	TTTTATCACT	GGAAGATTAC	TTGAAGGTGC	AAAAGATACT	TTGATTCGAC	ATGATGTTAA	3000
286	TGAAGACAAT	ATTGATGTAG	CATTTGTTCC	TGGTGCCTTT	GAAATTCCTT	TAGTAGCTAA	3060
287	AAAATTAGCC	TCATCAGGAA	ATTATGATGC	AATAATTACA	TTAGGATGCG	TAATTCGCGG	3120
288	TGCTACGTCT	CATTATGATT	ATGTTTGTA	TGAAGTGCGA	AAGGTGTTTC	TAAAGTAAAT	3180
289	GATCAAACCTA	ATGTACCAGT	CATATTTGGT	ATTTTAACGA	CTGAAAGTAT	TGAACAAGCT	3240
290	GTGGAAAGAG	CAGGTACGAA	AGCTGGTAAT	AAAGGTGCCG	AAGCAGCAGT	AAGTGCAATT	3300
291	GAAATGGCTA	ATTTATTAAA	ATCTATAAAA	GCATAG			3336

RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 3,13,23,37,44,45,114,118,142,147,161,179,184,775,898,998

Seq#:3; N Pos. 1011,1017,1179

Seq#:4; Xaa Pos.14,55,89,93,95

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/824,231

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Input Set : N:\Crf3\RULE60\10824231.raw

Output Set: N:\CRF4\08042004\J824231.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:34 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
M:341 Repeated in SeqNo=4